

STN.  
Registry File Search

Russel 09/876,257

June 21, 2003

=> b reg

FILE 'REGISTRY' ENTERED AT 13:58:40 ON 21 JUN 2003  
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.  
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.  
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Property values tagged with IC are from the ZIC/VINITI data file  
provided by InfoChem.

STRUCTURE FILE UPDATES: 20 JUN 2003 HIGHEST RN 534773-28-9  
DICTIONARY FILE UPDATES: 20 JUN 2003 HIGHEST RN 534773-28-9

TSCA INFORMATION NOW CURRENT THROUGH JANUARY 6, 2003

Please note that search-term pricing does apply when  
conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. See HELP  
PROPERTIES for more information. See STNote 27, Searching Properties  
in the CAS Registry File, for complete details:  
<http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf>

=> s hwsyxlrgqghwsyxlrg/sqsp

L1 0 HWSYXLRPGQHWSYXLRP/SQSP

=> d que

L1 0 SEA FILE=REGISTRY ABB=ON PLU=ON HWSYXLRPGQHWSYXLRP/SQSP

OM protein - protein search, using sw model

Run on: June 21, 2003, 16:21:25 ; Search time 77 Seconds  
(without alignments)  
48.167 Million cell updates/sec

Title: 09876257-4  
Perfect score: 105  
Sequence: 1 hwsyxlrgqhwsyxlrp 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_21.\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp Vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*

16: sp\_bacteriap:\*

17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query		%		DB	ID	Description
	Score	Match	Length				
1	56	53.3	90	13	Q90Y63		Q90y63 rana catesb
2	51	48.6	91	13	Q9PRH0		Q9prh0 anguilla ja
3	50	47.6	552	16	Q8XA02		Q8xa02 escherichia
4	49	46.7	187	16	Q8XW64		Q8xw64 ralstonia s
5	48	45.7	197	4	O00509		O00509 homo sapien
6	47	44.8	161	16	Q9RVD8		Q9rvd8 deinococcus
7	47	44.8	330	16	Q8YSM1		Q8ysm1 anabaena sp
8	46.5	44.3	148	16	Q8U5T2		Q8u5t2 agrobacteri
9	46	43.8	345	14	Q91UY7		Q91uy7 uncultured
10	46	43.8	491	16	Q8ZQR9		Q8zqr9 salmonella
11	46	43.8	491	16	Q8Z8A7		Q8z8a7 salmonella
12	46	43.8	512	11	Q9DAQ1		Q9daq1 mus musculu
13	45	42.9	87	13	Q9YI26		Q9yi26 sparus aura
14	45	42.9	96	13	Q8UW80		Q8uw80 verasper mo
15	45	42.9	242	16	Q9RZ29		Q9rz29 deinococcus
16	45	42.9	653	5	Q95V11		Q95v11 asterias ru
17	45	42.9	686	4	Q9H6R3		Q9h6r3 homo sapien
18	45	42.9	1713	5	Q9V3Q9		Q9v3q9 drosophila
19	45	42.9	4313	2	Q9L6D0		Q9l6d0 pseudomonas
20	44.5	42.4	341	11	P97775		P97775 rattus norv
21	44	41.9	279	16	Q9L156		Q9l156 streptomyce
22	44	41.9	379	10	Q9LV12		Q9lv12 arabidopsis
23	44	41.9	439	16	O53734		O53734 mycobacteri
24	44	41.9	482	2	Q9APV8		Q9apv8 pseudomonas
25	44	41.9	631	10	Q9SJ83		Q9sj83 arabidopsis
26	44	41.9	698	2	Q9KH03		Q9kh03 alcaligenes
27	44	41.9	708	2	Q46444		Q46444 comamonas t
28	44	41.9	740	10	Q9FZG5		Q9fzg5 arabidopsis
29	44	41.9	1277	10	Q9ZQQ6		Q9zqq6 arabidopsis
30	43.5	41.4	332	10	O22963		O22963 arabidopsis
31	43.5	41.4	907	16	Q93IX8		Q93ix8 streptomyce
32	43	41.0	186	16	Q55597		Q55597 synechocyst
33	43	41.0	275	2	P72114		P72114 pseudomonas

34	43	41.0	275	16	Q9I184	Q9i184 pseudomonas
35	43	41.0	277	5	Q20297	Q20297 caenorhabdi
36	43	41.0	351	11	Q99MV2	Q99mv2 mus musculu
37	43	41.0	421	5	Q9VC85	Q9vc85 drosophila
38	43	41.0	525	16	Q8XY77	Q8xy77 ralstonia s
39	43	41.0	528	16	Q8XXV7	Q8xxv7 ralstonia s
40	43	41.0	553	16	Q8ZIH3	Q8zih3 yersinia pe
41	43	41.0	561	10	Q9C6S8	Q9c6s8 arabidopsis
42	43	41.0	595	11	Q9Z206	Q9z206 mus musculu
43	43	41.0	730	5	O44766	O44766 caenorhabdi
44	42.5	40.5	637	16	Q9KRJ3	Q9krj3 vibrio chol
45	42	40.0	226	16	Q99YA8	Q99ya8 streptococc

## ALIGNMENTS

### RESULT 1

Q90Y63

ID Q90Y63 PRELIMINARY; PRT; 90 AA.

AC Q90Y63;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Gonadotropin-releasing hormone.

GN GNRH.

OS Rana catesbeiana (Bull frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.

OX NCBI\_TaxID=8400;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BRAIN;

RX MEDLINE=21102951; PubMed=11170016;

RA Wang L., Yoo M.S., Kang H.M., Im W.B., Choi H.S., Bogerd J.,

RA Kwon H.B.;

RT "Cloning and characterization of cDNAs encoding the GnRH1 and GnRH2

RT precursors from bullfrog (Rana catesbeiana).";

RL J. Exp. Zool. 289:190-201(2001).

DR EMBL; AF188754; AAL05972.1; -.

DR InterPro; IPR002012; GnRH.

DR Pfam; PF00446; GnRH; 1.

DR PROSITE; PS00473; GNRH; UNKNOWN\_1.

SQ SEQUENCE 90 AA; 10291 MW; 317203B4E3DA2FE7 CRC64;

Query Match 53.3%; Score 56; DB 13; Length 90;  
Best Local Similarity 90.0%; Pred. No. 0.16;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 GQHWSYXLRP 18

||||| |||  
Db 24 GQHWSYGLRP 33

Search completed: June 21, 2003, 16:27:29

Job time : 79 secs

OM protein - protein search, using sw model

Run on: June 21, 2003, 16:16:20 ; Search time 22 Seconds  
(without alignments)  
33.935 Million cell updates/sec

Title: 09876257-4  
Perfect score: 105  
Sequence: 1 hwsyxlrgqhwsyxlrp 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	% Query		Match	Length	DB	ID	Description
	Score						
1	51	48.6	61	1	GON1	SHEEP	Q28588 ovis aries
2	51	48.6	63	1	GON1	MESAU	O09163 mesocricetu
3	51	48.6	67	1	GON1	MACMU	P55247 macaca mula
4	51	48.6	89	1	GON1	XENLA	P45656 xenopus lae
5	51	48.6	90	1	GON1	MOUSE	P13562 mus musculu

6	51	48.6	91	1	GON1_PIG	P49921 sus scrofa
7	51	48.6	92	1	GON1_HUMAN	P01148 homo sapien
8	51	48.6	92	1	GON1_RAT	P07490 rattus norv
9	51	48.6	92	1	GON1_TUPGB	Q95335 tupaia glis
10	50	47.6	551	1	YABN_ECOLI	P33595 escherichia
11	49	46.7	90	1	GON8_RANDY	Q9iau2 rana dybows
12	47	44.8	10	1	GON1_ALLMI	P37041 alligator m
13	47	44.8	92	1	GON1_CAVPO	O54713 cavia porce
14	47	44.8	92	1	GON1_CHICK	P37042 gallus gall
15	47	44.8	584	1	GUND_CLOCE	P25472 clostridium
16	46	43.8	477	1	GUNA_CLOTM	P04955 clostridium
17	46	43.8	512	1	HYA1_MOUSE	P48794 mus musculu
18	45	42.9	94	1	GON1_HAPBU	P51918 haplochromi
19	45	42.9	95	1	GON1_MORSA	O73812 morone saxa
20	45	42.9	95	1	GON1_PAGMA	P70074 pagrus majo
21	45	42.9	95	1	GON1_SPAAU	P51919 sparus aura
22	45	42.9	99	1	GON1_DICLA	Q9ia10 dicentrarch
23	44	41.9	354	1	GAL7_STRLI	P13212 streptomyce
24	43.5	41.4	292	1	YB19_HAEIN	Q57273 haemophilus
25	43	41.0	1481	1	APU_THEET	P38939 t amylopull
26	42	40.0	450	1	AROA_MYCTU	P22487 mycobacteri
27	42	40.0	725	1	YJ76_YEAST	P47144 saccharomyc
28	42	40.0	919	1	NOS3_RAT	Q62600 rattus norv
29	41	39.0	80	1	GON1_CLAGA	P33439 clarias gar
30	41	39.0	261	1	AQP8_HUMAN	O94778 homo sapien
31	41	39.0	337	1	CAHE_HUMAN	Q9ulx7 homo sapien
32	41	39.0	728	1	HGF_HUMAN	P14210 homo sapien
33	41	39.0	900	1	GUNH_CLOTM	P16218 clostridium
34	40	38.1	10	1	GON1_CLUPA	P81749 clupea pall
35	40	38.1	110	1	YHBJ_ACTAC	P96769 actinobacil
36	40	38.1	248	1	COBK_RHOER	Q53139 rhodococcus
37	40	38.1	291	1	LGT_SALTY	Q07293 salmonella
38	40	38.1	431	1	KRE2_CANAL	Q00310 candida alb
39	40	38.1	452	1	MTEC_ENTCL	P14827 enterobacte
40	40	38.1	489	1	INGR_HUMAN	P15260 homo sapien
41	40	38.1	490	1	MODF_ECOLI	P31060 escherichia
42	40	38.1	728	1	HGF_MOUSE	Q08048 mus musculu
43	40	38.1	728	1	HGF_RAT	P17945 rattus norv
44	40	38.1	746	1	ABP_RAT	P36633 rattus norv
45	40	38.1	1420	1	APOA_MACMU	P14417 macaca mula

## ALIGNMENTS

RESULT 1

GON1\_SHEEP

ID GON1\_SHEEP STANDARD; PRT; 61 AA.

AC Q28588;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Progonadoliberin I precursor [Contains: Gonadoliberin I (LHRH I)

DE (Luteinizing hormone releasing hormone I) (Gonadotropin releasing

DE hormone I) (GnRH I) (Luliberin I); GnRH-associated peptide I]

DE (Fragment).

GN GNRH1 OR GNRH OR LHRH.

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Caprinae; Ovis.

OX NCBI\_TaxID=9940;

RN [1]

RP SEQUENCE OF 12-61 FROM N.A.

RC STRAIN=Western range; TISSUE=Hypothalamus;

RA Rodriguez R.E., Wise M.E.;

RL Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE OF 1-10.

RX MEDLINE=72094314; PubMed=4550508;

RA Burgus R., Butcher M., Amoss M., Ling N., Monahan M., Rivier J.,

RA Fellows R., Blackwell R., Vale W., Guillemin R.;

RT "Primary structure of the ovine hypothalamic luteinizing hormone-

RT releasing factor (LRF) (LH-hypothalamus-LRF-gas chromatography-mass

RT spectrometry-decapeptide-Edman degradation).";

RL Proc. Natl. Acad. Sci. U.S.A. 69:278-282(1972).

CC -!- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS; IT  
STIMULATES

CC THE SECRETION OF BOTH LUTEINIZING AND FOLLICLE-STIMULATING

CC HORMONES.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: BELONGS TO THE GNRH FAMILY.

CC -----

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).



CC -----  
 DR EMBL; U02517; AAA03433.1; -.  
 DR PIR; A93780; RHSHG.  
 DR InterPro; IPR002012; GnRH.  
 DR Pfam; PF00446; GnRH; 1.  
 DR PROSITE; PS00473; GNRH; 1.  
 KW Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;  
 KW Placenta.  
 FT NON\_TER 1 1  
 FT CHAIN 1 >61 PROGONADOLIBERIN I.  
 FT PEPTIDE 1 10 GONADOLIBERIN I.  
 FT PEPTIDE 14 >61 GNRH-ASSOCIATED PEPTIDE I.  
 FT ACT\_SITE 3 3 APPEARS TO BE ESSENTIAL FOR BIOLOGICAL  
 FT ACTIVITY.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 10 10 AMIDATION (G-11 PROVIDE AMIDE GROUP).  
 FT NON\_TER 61 61  
 SQ SEQUENCE 61 AA; 6828 MW; 63962A1AE319B8F0 CRC64;

Query Match 48.6%; Score 51; DB 1; Length 61;  
 Best Local Similarity 88.9%; Pred. No. 0.19;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HWSYXLRPG 9  
 |||| ||||  
 Db 2 HWSYGLRPG 10

Search completed: June 21, 2003, 16:26:03  
 Job time : 23 secs

OM protein - protein search, using sw model

Run on: June 21, 2003, 16:22:25 ; Search time 40 Seconds  
(without alignments)  
43.260 Million cell updates/sec

Title: 09876257-4  
Perfect score: 105  
Sequence: 1 hwsyxlrgqhwsyxlrp 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID	Description	
1	51	48.6	10	1	RHPGG	gonadoliberin - pi	

2	51	48.6	10	1	RHSHG	gonadoliberin - sh
3	51	48.6	67	2	I78541	gonadoliberin prec
4	51	48.6	89	2	I51423	gonadoliberin prec
5	51	48.6	90	1	RHMSG	gonadoliberin prec
6	51	48.6	92	1	RHHUG	gonadoliberin prec
7	51	48.6	92	1	RHRTG	gonadoliberin prec
8	50	47.6	551	2	E64728	yabN protein - Esc
9	50	47.6	552	2	B90638	probable transport
10	50	47.6	552	2	B85489	probable transport
11	47	44.8	10	1	RHAQ1	gonadoliberin I -
12	47	44.8	92	2	I50644	gonadoliberin I pr
13	47	44.8	161	2	C75438	hypothetical prote
14	47	44.8	330	2	AH2188	hypothetical prote
15	47	44.8	584	2	JQ1229	cellulase (EC 3.2.
16	46	43.8	477	1	CZCLAM	cellulase (EC 3.2.
17	46	43.8	491	2	AH0594	probable molybdenu
18	45	42.9	98	2	I50739	gonadotropin-relea
19	45	42.9	242	2	G75607	phosphoesterase-re
20	44	41.9	317	1	XNSMUD	UDPglucose-hexose-
21	44	41.9	439	2	B70831	probable dehydroge
22	44	41.9	631	2	B84461	hypothetical prote
23	44	41.9	708	2	S52317	quinohemoprotein e
24	44	41.9	740	2	A96519	protein T2E6.4 [im
25	44	41.9	1277	2	B84517	hypothetical prote
26	43.5	41.4	292	2	A64184	membrane protein l
27	43.5	41.4	332	2	D84752	hypothetical prote
28	43	41.0	186	2	S76125	hypothetical prote
29	43	41.0	275	2	F83347	hypothetical prote
30	43	41.0	277	2	B88690	protein F41H10.5 [
31	43	41.0	553	2	AC0065	conserved hypothet
32	43	41.0	561	2	H86442	unknown protein [i
33	43	41.0	730	2	F87803	protein bli-4B [im
34	43	41.0	1481	2	S28669	pullulanase (EC 3.
35	42.5	40.5	637	2	B82175	conserved hypothet
36	42	40.0	307	2	G75631	probable iron-chel
37	42	40.0	423	2	E82611	conserved hypothet
38	42	40.0	450	2	E70590	3-phosphoshikimate
39	42	40.0	565	2	G82443	conserved hypothet
40	42	40.0	700	2	B81682	conserved hypothet
41	42	40.0	725	2	S57127	probable membrane
42	41.5	39.5	711	2	T12525	hypothetical prote
43	41	39.0	80	1	RHID1S	gonadoliberin I pr
44	41	39.0	91	2	JC7393	medaka-type gonado
45	41	39.0	186	2	AB2081	hypothetical prote

## ALIGNMENTS

### RESULT 1

#### RHPGG

gonadoliberin - pig

C;Species: *Sus scrofa domestica* (domestic pig)

C;Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 18-Mar-1997

C;Accession: A01411

R;Baba, Y.; Matsuo, H.; Schally, A.V.

Biochem. Biophys. Res. Commun. 44, 459-463, 1971

A;Title: Structure of the porcine LH- and FSH-releasing hormone. II. Confirmation of the proposed structure by conventional sequential analyses.

A;Reference number: A90172; MUID:72114303; PMID:4946067

A;Accession: A01411

A;Molecule type: protein

A;Residues: 1-10 <BAB>

R;Matsuo, H.; Arimura, A.; Nair, R.M.G.; Schally, A.V.

Biochem. Biophys. Res. Commun. 45, 822-827, 1971

A;Title: Synthesis of the porcine LH- and FSH-releasing hormone by the solid-phase method.

A;Reference number: A90176; MUID:72065376; PMID:4942726

A;Contents: annotation; synthesis

A;Note: the synthetic and natural hormones have the same physicochemical and biological properties

R;Baba, Y.; Arimura, A.; Schally, A.V.

Biochem. Biophys. Res. Commun. 45, 483-487, 1971

A;Title: On the tryptophan residue in porcine LH and FSH-releasing hormone.

A;Reference number: A90175; MUID:72117544; PMID:4946275

A;Contents: annotation

A;Note: Trp-3 appears to be essential for biological activity

C;Comment: This hypothalamic hormone stimulates the secretion of both luteinizing and follicle-stimulating hormones.

C;Superfamily: gonadoliberin

C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 48.6%; Score 51; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 0.1;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HWSYXLRPG 9

|||||

Db 2 HWSYGLRPG 10

#### RESULT 4

I51423

gonadoliberin precursor - African clawed frog

N;Alternate names: luteinizing hormone releasing hormone

C;Species: *Xenopus laevis* (African clawed frog)

C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Jul-1999

C;Accession: I51423

R;Hayes, W.P.; Wray, S.; Battey, J.F.

Endocrinology 134, 1835-1845, 1994

A;Title: The frog GnRH-I gene has a mammalian-like expression pattern and conserved domains in GnRH-associated peptide, but brain onset is delayed until metamorphosis.

A;Reference number: I51423; MUID:94185563; PMID:8137750

A;Accession: I51423

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-89 <HAY>

A;Cross-references: GB:L28040; NID:g496291; PIDN:AAA49728.1; PID:g496292

C;Genetics:

A;Gene: GnRH-I

C;Superfamily: gonadoliberin

Query Match 48.6%; Score 51; DB 2; Length 89;

Best Local Similarity 52.9%; Pred. No. 0.89;

Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 2 WSYXLRPGQHWSYXLRP 18

:| : ||||| |||

Db 16 FSAHVSDAQHWSYGLRP 32

Search completed: June 21, 2003, 16:28:16

Job time : 42 secs

OM protein - protein search, using sw model

Run on: June 21, 2003, 16:27:36 ; Search time 47 Seconds  
(without alignments)  
41.441 Million cell updates/sec

Title: 09876257-4  
Perfect score: 105  
Sequence: 1 hwsyxlrgqhwsyxlrp 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		%					
Result	Query						
No.	Score	Match	Length	DB	ID	Description	
1	101	96.2	20	9	US-09-964-201A-26	Sequence 26, Appl	
2	101	96.2	20	9	US-09-964-201A-30	Sequence 30, Appl	
3	101	96.2	40	9	US-09-964-201A-35	Sequence 35, Appl	
4	101	96.2	41	9	US-09-964-201A-34	Sequence 34, Appl	
5	98	93.3	20	9	US-09-964-201A-29	Sequence 29, Appl	
6	98	93.3	20	9	US-09-964-201A-31	Sequence 31, Appl	
7	83.5	79.5	695	9	US-09-305-924-13	Sequence 13, Appl	
8	83	79.0	49	9	US-09-305-924-11	Sequence 11, Appl	
9	83	79.0	49	10	US-09-019-010-4	Sequence 4, Appli	
10	73	69.5	46	10	US-09-848-834A-19	Sequence 19, Appl	
11	72.5	69.0	47	10	US-09-848-834A-17	Sequence 17, Appl	
12	71	67.6	50	10	US-09-848-834A-18	Sequence 18, Appl	
13	70.5	67.1	51	10	US-09-848-834A-20	Sequence 20, Appl	
14	52	49.5	16	9	US-09-305-924-5	Sequence 5, Appli	
15	52	49.5	28	10	US-09-848-834A-11	Sequence 11, Appl	
16	52	49.5	383	10	US-09-147-346-2	Sequence 2, Appli	
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18	51	48.6	10	9	US-09-810-601-1	Sequence 1, Appli	
19	51	48.6	10	9	US-10-184-126-1	Sequence 1, Appli	
20	51	48.6	10	9	US-10-115-553-1	Sequence 1, Appli	
21	51	48.6	10	9	US-10-122-483-1	Sequence 1, Appli	
22	51	48.6	10	9	US-09-305-924-1	Sequence 1, Appli	
23	51	48.6	10	9	US-09-305-924-9	Sequence 9, Appli	
24	51	48.6	10	9	US-09-964-201A-28	Sequence 28, Appl	
25	51	48.6	10	9	US-09-964-201A-32	Sequence 32, Appl	
26	51	48.6	10	10	US-09-019-010-2	Sequence 2, Appli	
27	51	48.6	11	9	US-10-044-034-17	Sequence 17, Appl	
28	51	48.6	14	9	US-09-305-924-2	Sequence 2, Appli	
29	51	48.6	17	9	US-09-305-924-3	Sequence 3, Appli	
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31	51	48.6	31	10	US-09-848-834A-15	Sequence 15, Appl	
32	51	48.6	34	10	US-09-848-834A-13	Sequence 13, Appl	
33	51	48.6	36	10	US-09-848-834A-16	Sequence 16, Appl	
34	51	48.6	37	10	US-09-848-834A-14	Sequence 14, Appl	
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36	50	47.6	33	10	US-09-848-834A-12	Sequence 12, Appl	

37	50	47.6	34	10	US-09-848-834A-10	Sequence 10, Appl
38	50	47.6	260	10	US-09-925-300-1314	Sequence 1314, Ap
39	47	44.8	10	9	US-10-054-552-1	Sequence 1, Appli
40	45	42.9	10	9	US-10-109-331-2	Sequence 2, Appli
41	45	42.9	10	9	US-09-810-601-2	Sequence 2, Appli
42	45	42.9	10	9	US-09-810-601-3	Sequence 3, Appli
43	45	42.9	10	9	US-09-810-601-4	Sequence 4, Appli
44	45	42.9	10	9	US-09-810-601-5	Sequence 5, Appli
45	45	42.9	10	9	US-09-810-601-6	Sequence 6, Appli

## ALIGNMENTS

### RESULT 1

US-09-964-201A-26

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; Sequence 26, Application US/09964201A
; Publication No. US20030091575A1
; GENERAL INFORMATION:
; APPLICANT: Kenten, John H
; APPLICANT: Tramontano, Alfonso
; APPLICANT: Pilon, Aprile L
; APPLICANT: Lohnas, Gerald L
; APPLICANT: Roberts, Steven F
; TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM
; FILE REFERENCE: U.S. Patent Application No. US20030091575A1 09\026,276
; CURRENT APPLICATION NUMBER: US/09/964,201A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Porcine
US-09-964-201A-26
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Query Match 96.2%; Score 101; DB 9; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 4.6e-08;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db      2 HWSYGLRPGQHWSYGLRP 19
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RESULT 7

US-09-305-924-13

; Sequence 13, Application US/09305924A

; Publication No. US20030091579A1

; GENERAL INFORMATION:

; APPLICANT: Jack G. Manns

; APPLICANT: Stephen D. Acres

; APPLICANT: Richard Harland

; TITLE OF INVENTION: METHODS OF RAISING ANIMALS FOR MEAT PRODUCTION

; FILE REFERENCE: 9001-0048

; CURRENT APPLICATION NUMBER: US/09/305,924A

; CURRENT FILING DATE: 1999-05-05

; EARLIER APPLICATION NUMBER: US 60/084,217

; EARLIER FILING DATE: 1998-05-05

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 13

; LENGTH: 695

; TYPE: PRT

; ORGANISM: GnRH

US-09-305-924-13

Query Match 79.5%; Score 83.5; DB 9; Length 695;

Best Local Similarity 48.5%; Pred. No. 0.00041;

Matches 16; Conservative 0; Mismatches 2; Indels 15; Gaps 1;

Qy 1 HWSYXLRPG-----QHWSYXLRP 18

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Db 36 HWSYGLRPGSGSQDWSYGLRPGGSQHWSYGLRP 68

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Run on: June 21, 2003, 16:24:25 ; Search time 26 Seconds  
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Title: 09876257-4  
Perfect score: 105  
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Scoring table: BLOSUM62  
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Searched: 262574 seqs, 29422922 residues

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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Result	Query	
No.	Score Match Length DB ID	Description

1	101	96.2	20	4	US-09-026-276-26	Sequence 26, Appl
2	101	96.2	20	4	US-09-026-276-30	Sequence 30, Appl
3	101	96.2	40	4	US-09-026-276-35	Sequence 35, Appl
4	101	96.2	41	4	US-09-026-276-34	Sequence 34, Appl
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6	98	93.3	20	4	US-09-026-276-29	Sequence 29, Appl
7	98	93.3	20	4	US-09-026-276-31	Sequence 31, Appl
8	98	93.3	24	1	US-07-690-983D-43	Sequence 43, Appl
9	98	93.3	44	1	US-07-690-983D-45	Sequence 45, Appl
10	98	93.3	52	3	US-08-458-814-6	Sequence 6, Appli
11	98	93.3	55	3	US-08-458-814-7	Sequence 7, Appli
12	98	93.3	84	1	US-07-690-983D-47	Sequence 47, Appl
13	83.5	79.5	699	2	US-08-694-865-16	Sequence 16, Appl
14	83.5	79.5	699	3	US-09-124-491-16	Sequence 16, Appl
15	83	79.0	49	1	US-08-387-156-4	Sequence 4, Appli
16	83	79.0	49	2	US-08-694-865-4	Sequence 4, Appli
17	83	79.0	49	2	US-08-878-748-4	Sequence 4, Appli
18	83	79.0	49	3	US-09-124-491-4	Sequence 4, Appli
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22	83	79.0	544	3	US-09-124-491-10	Sequence 10, Appl
23	83	79.0	977	1	US-08-387-156-8	Sequence 8, Appli
24	83	79.0	977	2	US-08-694-865-8	Sequence 8, Appli
25	83	79.0	977	2	US-08-878-748-8	Sequence 8, Appli
26	83	79.0	977	3	US-09-124-491-8	Sequence 8, Appli
27	61	58.1	17	1	US-07-690-983D-16	Sequence 16, Appl
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35	58	55.2	18	4	US-09-315-304B-1173	Sequence 1173, Ap
36	58	55.2	30	3	US-09-100-414B-67	Sequence 67, Appl
37	58	55.2	30	4	US-09-303-323-67	Sequence 67, Appl
38	56	53.3	30	3	US-09-100-414B-70	Sequence 70, Appl
39	56	53.3	30	4	US-09-303-323-70	Sequence 70, Appl
40	53	50.5	10	1	US-07-690-983D-37	Sequence 37, Appl
41	53	50.5	26	1	US-08-446-692-29	Sequence 29, Appl
42	53	50.5	26	2	US-08-488-351A-29	Sequence 29, Appl
43	53	50.5	27	1	US-08-446-692-19	Sequence 19, Appl
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# ALIGNMENTS

## RESULT 1

US-09-026-276-26

; Sequence 26, Application US/09026276

; Patent No. 6319503

; GENERAL INFORMATION:

; APPLICANT: Kenten, John H

; APPLICANT: Tramontano, Alfonso

; APPLICANT: Pilon, Aprile L

; APPLICANT: Lohnas, Gerald L

; APPLICANT: Roberts, Steven F

; TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM

; FILE REFERENCE: U.S. Patent Application No. 6319503 09\026,276

; CURRENT APPLICATION NUMBER: US/09/026,276

; CURRENT FILING DATE: 1998-02-19

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 26

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Porcine

US-09-026-276-26

Query Match 96.2%; Score 101; DB 4; Length 20;  
Best Local Similarity 88.9%; Pred. No. 4e-09;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 2 HWSYGLRPGQHWSYGLRP 19

## RESULT 5

US-07-690-983D-40

; Sequence 40, Application US/07690983D

; Patent No. 5403586

; GENERAL INFORMATION:

; APPLICANT: RUSSELL-JONES, Gregory J.

; APPLICANT: STEWART, Andrew G.

; APPLICANT: TSONIS, Con G.

; TITLE OF INVENTION: FUSION PROTEINS  
 ; NUMBER OF SEQUENCES: 47  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 3000 K Street, N.W.  
 ; CITY: Washington, D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/690,983D  
 ; FILING DATE: 25-JUN-1991  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/AU90/00373  
 ; FILING DATE: 24-AUG-1990  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BENT, Stephen A.  
 ; REGISTRATION NUMBER: 29,768  
 ; REFERENCE/DOCKET NUMBER: 16786/148 CHAC  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202)672-5300  
 ; TELEFAX: (202)672-5399  
 ; INFORMATION FOR SEQ ID NO: 40:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 20 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-07-690-983D-40

Query Match 93.3%; Score 98; DB 1; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 1.1e-08;  
 Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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 Db 3 HWSYGLRPGEHWSYGLRP 20

RESULT 10

US-08-458-814-6

; Sequence 6, Application US/08458814

; Patent No. 6103243

; GENERAL INFORMATION:

; APPLICANT: RUSSELL-JONES, Gregory J

; APPLICANT: DE AIZPURUA, Henry J

; APPLICANT: HOWE, Peter

; APPLICANT: RAND, Keith N

; TITLE OF INVENTION: ORAL VACCINES

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/458,814

; FILING DATE: 02-JUN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/327,822

; FILING DATE: 18-OCT-1994

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/AU86/00135

; FILING DATE: 14-MAY-1986

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: AU PH3104

; FILING DATE: 25-OCT-1985

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: AU PH0566

; FILING DATE: 15-MAY-1985

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 60042/155/BIAU

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202 672 5300

; TELEFAX: 202 672 5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 52 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-458-814-6

Query Match 93.3%; Score 98; DB 3; Length 52;  
Best Local Similarity 83.3%; Pred. No. 3e-08;  
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db 17 HWSYGLRPGEHWSYGLRP 34

#### RESULT 13

US-08-694-865-16

; Sequence 16, Application US/08694865  
; Patent No. 5837268  
; GENERAL INFORMATION:  
; APPLICANT: POTTER, ANDREW A.  
; APPLICANT: MANNS, JOHN G.  
; TITLE OF INVENTION: GnRH-LEUKOTOXIN CHIMERAS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: REED & ROBINS LLP  
; STREET: 285 HAMILTON AVENUE, SUITE 200  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/694,865  
; FILING DATE: 09-AUG-1996  
; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:  
; NAME: MCCracken, THOMAS P.  
; REGISTRATION NUMBER: 38,548  
; REFERENCE/DOCKET NUMBER: 9001-0016.22  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415)327-3400  
; TELEFAX: (415)327-3231  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 699 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-694-865-16

Query Match 79.5%; Score 83.5; DB 2; Length 699;  
Best Local Similarity 48.5%; Pred. No. 6e-05;  
Matches 16; Conservative 0; Mismatches 2; Indels 15; Gaps 1;

Qy 1 HWSYXLRPG-----QHWSYXLRP 18  
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Db 36 HWSYGLRPGSGSQDWSYGLRPGGSQHWSYGLRP 68

RESULT 14

US-09-124-491-16

; Sequence 16, Application US/09124491  
; Patent No. 6022960  
; GENERAL INFORMATION:  
; APPLICANT: POTTER, ANDREW A.  
; APPLICANT: MANNS, JOHN G.  
; TITLE OF INVENTION: GnRH-LEUKOTOXIN CHIMERAS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: REED & ROBINS LLP  
; STREET: 285 HAMILTON AVENUE, SUITE 200  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30



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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/124,491
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/694,865
; FILING DATE: 09-AUG-1996
; APPLICATION NUMBER: US 08/387,156
; FILING DATE: 10-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,932
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/779,171
; FILING DATE: 16-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 9001-0016.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)327-3400
; TELEFAX: (415)327-3231
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 699 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-124-491-16

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Query Match 79.5%; Score 83.5; DB 3; Length 699;  
 Best Local Similarity 48.5%; Pred. No. 6e-05;  
 Matches 16; Conservative 0; Mismatches 2; Indels 15; Gaps 1;

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Db      36 HWSYGLRPGSGSQDWSYGLRPGGSQHWSYGLRP 68

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RESULT 15  
 US-08-387-156-4  
 ; Sequence 4, Application US/08387156  
 ; Patent No. 5723129  
 ; GENERAL INFORMATION:  
 ; APPLICANT: POTTER, ANDREW A.

; APPLICANT: REDMOND, MARK J.  
 ; APPLICANT: HUGHES, HUW P.A.  
 ; TITLE OF INVENTION: GnRH-LEUKOTOXIN CHIMERAS  
 ; NUMBER OF SEQUENCES: 28  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: REED & ROBINS  
 ; STREET: 635 BRYANT STREET  
 ; CITY: PALO ALTO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: UNITED STATES OF AMERICA  
 ; ZIP: 94301  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
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 ; FILING DATE: 10-FEB-1995  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/960,932  
 ; FILING DATE: 14-OCT-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/779,171  
 ; FILING DATE: 16-OCT-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: ROBINS, ROBERTA L.  
 ; REGISTRATION NUMBER: 33,208  
 ; REFERENCE/DOCKET NUMBER: 9001-0016.21  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 617-8999  
 ; TELEFAX: (415) 327-3231  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 49 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-387-156-4

Query Match 79.0%; Score 83; DB 1; Length 49;  
 Best Local Similarity 47.1%; Pred. No. 4.8e-06;  
 Matches 16; Conservative 0; Mismatches 2; Indels 16; Gaps 1;

Qy 1 HWSYXLRPG-----QHWSYXLRP 18  
|||| ||| |||| |||  
Db 2 HWSYGLRPGSGSQDWSYGLRPGGSSQHWSYGLRP 35

Search completed: June 21, 2003, 16:28:48  
Job time : 27 secs

OM protein - protein search, using sw model

Run on: June 21, 2003, 16:15:45 ; Search time 70 Seconds  
(without alignments)  
34.264 Million cell updates/sec

Title: 09876257-4  
Perfect score: 105  
Sequence: 1 hwsyxlrgqhwsyxlrp 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_101002.\*  
1: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*  
2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*  
3: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:\*  
4: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:\*  
5: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:\*  
6: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:\*  
7: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:\*  
8: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:\*  
9: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:\*  
10: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:\*  
11: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:\*  
12: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:\*  
13: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:\*  
14: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:\*  
15: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:\*

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 22: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:\*  
 23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result	% Query						Description
	No.	Score	Match	Length	DB	ID	
1	103	98.1	21	23	ABB76119		G6A-GnRH-tandem pe
2	101	96.2	20	19	AAW47438		Antigenic peptide.
3	101	96.2	20	20	AAY31174		Ubiquitin fusion p
4	101	96.2	20	20	AAY31178		Ubiquitin fusion p
5	101	96.2	20	22	AAB71945		GnRH dimer. Unide
6	101	96.2	20	22	AAB71949		GnRH mixed dimer p
7	101	96.2	20	23	ABB76104		Gonadotropin relea
8	101	96.2	21	11	AAR07324		Luteinising hormon
9	101	96.2	21	18	AAW21648		Peptide containing
10	101	96.2	21	23	ABB76105		G6k-GnRH-tandem pe
11	101	96.2	21	23	ABB76107		G6k-GnRH-tandem pe
12	101	96.2	21	23	ABB76112		G6k-GnRH-tandem pe
13	101	96.2	21	23	ABB76113		GnRH-tandem peptid
14	101	96.2	30	11	AAR07323		Luteinising hormon
15	101	96.2	40	20	AAY31183		Ubiquitin fusion p
16	101	96.2	40	22	AAB71954		GnRH sequence #2.
17	101	96.2	41	20	AAY31182		Ubiquitin fusion p
18	101	96.2	41	22	AAB71953		GnRH sequence #1.
19	101	96.2	42	18	AAW21649		Peptide containing
20	101	96.2	42	21	AAB20865		GnRH tandem dimer
21	101	96.2	42	23	ABB76106		D-Lys6-tandem-GnRH
22	101	96.2	44	18	AAW21650		Peptide containing
23	98	93.3	20	20	AAY31177		Ubiquitin fusion p
24	98	93.3	20	20	AAY31179		Ubiquitin fusion p
25	98	93.3	20	22	AAB71948		GnRH dimer peptide
26	98	93.3	20	22	AAB71950		GnRH mixed dimer p
27	98	93.3	40	21	AAY96085		Cattle gonadotropi

28	98	93.3	263	12	AAR11185	Plasmid pBTA870-en
29	98	93.3	283	12	AAR11186	Plasmid pBTA862-en
30	98	93.3	323	12	AAR11187	Plasmid pBTA859-en
31	98	93.3	398	21	AAAY96090	BHV-1 truncated gD
32	98	93.3	399	21	AAAY96093	BHV-1 truncated gD
33	98	93.3	411	21	AAAY96089	GnRH tetramer-trun
34	98	93.3	442	21	AAAY96091	GnRH tetramer-BHV-
35	95	90.5	21	23	ABB76100	Peptide S4A-G6k-Gn
36	95	90.5	21	23	ABB76102	Peptide G10A-G6k-G
37	95	90.5	21	23	ABB76108	pE1A-G6K-GnRH-tand
38	95	90.5	21	23	ABB76114	pE1A-GnRH-tandem p
39	95	90.5	21	23	ABB76117	S4A-GnRH-tandem pe
40	95	90.5	21	23	ABB76123	G10A-GnRH-tandem p
41	91	86.7	21	23	ABB76110	L7A-G6K-GnRH-tande
42	91	86.7	21	23	ABB76120	L7A-GnRH-tandem pe
43	89	84.8	21	23	ABB76101	Peptide R8A-G6k-Gn
44	89	84.8	21	23	ABB76121	R8A-GnRH-tandem pe
45	86.5	82.4	23	21	AAB20864	GnRH tandem repeat

## ALIGNMENTS

### RESULT 1

ABB76119

ID ABB76119 standard; Peptide; 21 AA.

XX

AC ABB76119;

XX

DT 15-JUL-2002 (first entry)

XX

DE G6A-GnRH-tandem peptide.

XX

KW Gonadotropin releasing hormone; GnRH; vaccine; prostate cancer;

KW immunocastration; cytostatic; anabolic.

XX

OS Mammalia.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 6

FT /note= "wild-type Gly substituted by Ala"

FT Misc-difference 16

FT /note= "wild-type Gly substituted by Ala"

FT Misc-difference 21

FT /note= "C-terminal amide"

XX

PN WO200222659-A2.

XX

PD 21-MAR-2002.

XX

PF 11-SEP-2001; 2001WO-NL00666.

XX

PR 12-SEP-2000; 2000US-0659983.

XX

PA (IDLE-) ID-LELYSTAD INST DIERHOUDERIJ EN DIERGEZ.

XX

PI Meloen RH, Oonk HB, Turkstra JA;

XX

DR WPI; 2002-393944/42.

XX

PT Peptide for treating prostate cancer and immunocastration, comprises  
PT modified gonadotropin releasing hormone decapeptide sequence which  
PT allows for immunogenic response that allows for discrimination between  
PT different types of GnRH -

XX

PS Disclosure; Page 33; 43pp; English.

XX

CC The present sequence is that of an alanine-replacement peptide of  
CC a mammalian gonadotropin releasing hormone I (GnRH-I) tandem  
CC repeat peptide (see ABB76113). The GnRH-I-tandem repeat, and  
CC alanine-replacement derivatives of it (see ABB76114-23), were  
CC dimerised and conjugated to ovalbumin. The peptides were tested  
CC for efficacy for immunocastration of pigs. High efficacy was found  
CC for S4A and G10A GnRH-tandem peptides, with moderate efficacy for  
CC the present G6A peptide. Preferred modified, GnRH-I-tandem peptides  
CC (see ABB76100-02) are used in vaccines to reduce testis growth and  
CC to reduce testosterone to non-detectable levels. A single dose of  
CC a claimed vaccine is effective for the immunocastration of pigs.  
CC Vaccines comprising the modified GnRH-I-tandem peptides can also be  
CC used to alter the reproduction or behaviour of a mammal, e.g. to  
CC sterilise domestic animals, to treat aggressiveness in males, to  
CC prevent or treat restlessness in male animals being fattened for  
CC slaughter, and to improve meat quality in pigs. The peptide gives  
CC an immunogenic response that allows for effective discrimination  
CC between GnRH-I and GnRH-II. In humans, immunisation against GnRH,  
CC preferably selective against either GnRH-I or GnRH-II, could be used  
CC in the treatment of prostate cancer (claimed), breast cancer and  
CC some forms of pituitary carcinoma.

XX

SQ Sequence 21 AA;

Query Match 98.1%; Score 103; DB 23; Length 21;  
Best Local Similarity 88.9%; Pred. No. 1.2e-08;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HWSYXLRPGQHWSYXLRP 18  
||||| ||||| |||  
Db 2 HWSYALRPGQHWSYALRP 19

## RESULT 2

AAW47438

ID AAW47438 standard; peptide; 20 AA.

XX

AC AAW47438;

XX

DT 05-JUN-1998 (first entry)

XX

DE Antigenic peptide.

XX

KW Vaccine; antigen.

XX

OS Synthetic.

XX

PN WO9749425-A1.

XX

PD 31-DEC-1997.

XX

PF 24-JUN-1997; 97WO-NL00354.

XX

PR 25-JUN-1996; 96EP-0201766.

XX

PA (DAVE-) DANISH VETERINARY INST ANIMAL VIRUS RES.

PA (DIER-) STICHTING INST DIERHOUDERIJ EN DIERGEZONHEID.

XX

PI Beekman NJCM, Dalsgaard K, Meloen RH, Schaaper WMM;

XX

DR WPI; 1998-076912/07.

XX

PT Vaccines comprising antigen bound to carrier by an in vivo labile

PT bond - especially synthetic peptide linked to fatty acid via

PT thioester or di: sulphide, provide greater immune response for weakly

PT immunogenic antigens

XX



PS Claim 9; Page 28; 36pp; English.

XX

CC A novel vaccine comprises an antigen (Ag), e.g. the present  
CC peptide, and carrier connected by a bond that is labile and  
CC dissociates under certain physiological conditions.  
CC The vaccine, which allows dissociation of the Ag from the carrier  
CC molecule, can be used to elicit better immune responses against  
CC poorly immunogenic Ag then those Ag which contain a stable link to  
CC the carrier molecule. Ag dissociate from the carrier in vivo,  
CC resulting in better immune response for Ag that are normally only  
CC weakly immunogenic. The vaccine also improves targetting to, and  
CC presentation by Ag-presenting cells.

XX

SQ Sequence 20 AA;

Query Match 96.2%; Score 101; DB 19; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2.3e-08;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HWSYXLRPGQHWSYXLRP 18  
||| ||||| |||  
Db 2 HWSYGLRPGQHWSYGLRP 19

### RESULT 3

AAY31174

ID AAY31174 standard; peptide; 20 AA.

XX

AC AAY31174;

XX

DT 28-OCT-1999 (first entry)

XX

DE Ubiquitin fusion protein GnRH dimer for C-terminal extension.

XX

KW Ubiquitin; immunocastration; fusion protein; heat shock protein; epitope;  
KW immune response stimulation; vaccine; T cell; viral; infection; cancer;  
KW bacterial; parasitic; treatment; gastrointestinal disease; HIV infection;  
KW pulmonary inflection; respiratory inflection; scaffold; anti-self; pig;  
KW steridogenesis; gamete maturation; prostate; breast; castration; TNF;  
KW tumour necrosis factor; septic shock; arthritis; Crohn's disease;  
KW inflammatory bowel disease; ulcerative colitis; chorionic gonadotropin;  
KW fertility; sperm protein; growth rate; antibody; detection; GnRH.

XX

OS Synthetic.

XX

PN WO9942472-A1.

XX

PD 26-AUG-1999.

XX

PF 26-JAN-1999; 99WO-US01588.

XX

PR 19-FEB-1998; 98US-0026276.

XX

PA (IGEN-) IGEN INT INC.

XX

PI Kenten JH, Lohnas GL, Pilon AL, Roberts SF, Tramontano A;

XX

DR WPI; 1999-518582/43.

XX

PT Epitope-containing fusion proteins used to generate a highly

PT specific immune responses

XX

PS Example 3; Page 40; 67pp; English.

XX

CC This invention describes a novel fusion protein, comprising a heat shock  
CC protein (e.g. ubiquitin), fused to an epitope(s) in a defined manner  
CC which is useful for the stimulation of a highly specific immune response  
CC when administered to an animal. The protein of the invention may be  
CC post-translationally modified (e.g. by the addition of fatty acids to  
CC enhance immunogenicity). The fusion proteins of the invention can be  
CC used as vaccines to induce an immune response. When a T cell epitope is  
CC attached, they can be used for control of viral infections, bacterial  
CC infections, parasitic infection and cancer. The fusion proteins can be  
CC used in pharmaceutical compositions for the treatment of gastrointestinal  
CC diseases, pulmonary infections, respiratory infections, and HIV  
CC infections. The use of ubiquitin as a scaffold is also useful for the  
CC presentation and stimulation of anti-self immune responses, e.g.  
CC generation of anti-gonadotropin releasing hormone antibodies which result  
CC in the suppression of luteinizing hormone and follicle stimulating  
CC hormone. This indirectly suppresses steroidogenesis and gamete maturation  
CC in males and females. This type of anti-self response in humans is useful  
CC in the treatment of prostate cancer and breast cancer. In livestock, the  
CC ability to stimulate an anti-self response provides a simple alternative  
CC to physical castration. Immunocastration of pigs is a better alternative  
CC to physical castration, as it does not result in any of the detrimental  
CC side effects associated with physical castration. Other examples of  
CC diseases and conditions treated with self proteins fused with ubiquitin  
CC are TNF and its epitopes to modulate septic shock, arthritis,  
CC inflammatory bowel disease, Crohn's disease, and ulcerative colitis; Ig  
CC epsilon heavy chain for the control of allergic reactions; chorionic

CC gonadotropin for fertility control; and sperm proteins for fertility  
CC control. A further use of the fusion proteins is as part of a vaccine to  
CC enhance growth rate and thereby the final weight of the livestock prior  
CC to shipment to market. In addition, the fusion proteins of the invention  
CC can be used to detect and identify antibodies from experimental samples.  
CC This sequence represents a GnRH dimer used in the construction of a  
CC ubiquitin fusion protein described in the method of the invention.

XX

SQ Sequence 20 AA;

Query Match 96.2%; Score 101; DB 20; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2.3e-08;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HWSYXLRPGQHWSYXLRP 18  
||| ||||| |||  
Db 2 HWSYGLRPGQHWSYGLRP 19

## RESULT 5

AAB71945

ID AAB71945 standard; Peptide; 20 AA.

XX

AC AAB71945;

XX

DT 10-MAY-2001 (first entry)

XX

DE GnRH dimer.

XX

KW GnRH; gonadotrophin releasing hormone; immunostimulant; antiallergic;

KW growth promoting; vaccine; heat shock fusion protein; ubiquitin;

KW self-epitope; immunogen; male-specific peptide hormone;

KW female-specific peptide hormone.

XX

OS Unidentified.

XX

PN WO200112216-A1.

XX

PD 22-FEB-2001.

XX

PF 14-AUG-2000; 2000WO-US22121.

XX

PR 13-AUG-1999; 99US-0374721.

XX

PA (PROT-) PROTEINIX CO.

XX

PR 13-AUG-1999; 99US-0374721.

XX

PA (PROT-) PROTEINIX CO.

XX

PI Kenten JH, Roberts S, Lohnas G;

XX

DR WPI; 2001-202829/20.

XX

PT Novel fusion proteins for stimulating immune response in animals

PT against self-antigen, has heat shock protein fused to single or a group

PT of epitope-containing segments having identical or non-identical self

PT epitopes -

XX

PS Claim 14; Page 63; 94pp; English.

XX

CC The present sequence is given in an example illustrating an invention  
CC disclosing self-epitope-containing heat shock fusion proteins. The  
CC proteins comprise a heat shock protein, preferably ubiquitin, fused to a  
CC single epitope-containing segment or two or more non-contiguous epitope  
CC containing segments, each epitope-containing segment comprising one or  
CC more identical or non-identical self-epitopes. The heat shock fusion  
CC proteins are useful for stimulating an immune response in an animal,  
CC especially a pig, directed towards a self-antigen, in particular a male  
CC or female-specific peptide hormone. The physiological consequence is  
CC substantially similar to the consequences of surgical castration. The  
CC proteins are useful for identifying antibodies in experimental or  
CC diagnostic samples and for reducing levels of a predetermined endogenous  
CC protein, such as gonadotropin releasing hormone, tumour necrosis factor  
CC or growth hormone protein. They are also useful for reducing allergic  
CC response and for increasing the growth rate of an animal. The proteins  
CC have a high specific immune response and do not result in detrimental  
CC side-effects.

XX

SQ Sequence 20 AA;

Query Match 96.2%; Score 101; DB 22; Length 20;

Best Local Similarity 88.9%; Pred. No. 2.3e-08;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HWSYXLRPGQHWSYXLRP 18

||||| ||||| |||

Db 2 HWSYGLRPGQHWSYGLRP 19

RESULT 8

AAR07324

ID AAR07324 standard; protein; 21 AA.

XX

AC AAR07324;

XX

DT 29-JAN-1991 (first entry)

XX

DE Luteinising hormone releasing hormone derived peptide.

XX

KW LHRH; vaccine; meat; pigs; cancer; sterilisation.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /label=OTHER

FT /note="OTHER=pyroglutamic acid

FT Modified-site 3

FT /label=OTHER

FT /note="OTHER= N-formyl-Trp (optional)"

FT Modified-site 13

FT /label=OTHER

FT /note="OTHER= N-formyl-Trp (optional)"

FT Misc-difference 21

FT /label=OTHER

FT /note="OTHER=Cys-NH2

XX

PN WO9011298-A.

XX

PD 04-OCT-1990.

XX

PF 22-MAR-1990; 90WO-NL00037.

XX

PR 23-MAR-1989; 89NL-0000726.

XX

PA (DIER-) STICHT CENT DIERGEN.

XX

PI Meloen RH, Wensing CJG;

XX

DR WPI; 1990-320228/42.

XX

PT Peptide for vaccinating mammals against LHRH - comprises at least

PT two luteinising hormone releasing hormone sequences in tandem

XX

PS Claim 4; Page 10; 15pp; English.

XX

CC The peptide comprises at least 2 LHRH sequences in tandem. The

CC peptide can be used to vaccinate mammals (e.g. pigs) against LHRH.

CC Such vaccination is used in human medicine for the treatment of

CC prostate cancer and breast cancer and some forms of hypophyseal

CC carcinoma. Other applicns. include sterilisation of domestic

CC animals and treatment of aggression in dogs. A major use of the

CC vaccination is to improve meat quality in pigs by avoiding "boar

CC odour" associated with the meat of sexually mature pigs.

CC See also AAR07323.

XX

SQ Sequence 21 AA;

Query Match 96.2%; Score 101; DB 11; Length 21;

Best Local Similarity 88.9%; Pred. No. 2.4e-08;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HWSYXLRPGQHWSYXLRP 18

|||||

Db 2 HWSYGLRPGQHWSYGLRP 19

#### RESULT 9

AAW21648

ID AAW21648 standard; peptide; 21 AA.

XX

AC AAW21648;

XX

DT 27-AUG-1997 (first entry)

XX

DE Peptide containing two contiguous LHRH decapeptides.

XX

KW Luteinising hormone releasing hormone; LHRH; decapeptide;

KW vaccine; reproductive characteristic; behavioural characteristic;

KW porcine; immunocastration; immunisation; prostate cancer;

KW breast cancer; pituitary carcinoma.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /label= OTHER

FT /note= "pyroglutamic acid"  
FT Misc-difference 6  
FT /note= "Gly or a dextrorotatory amino acid with a  
FT side chain that can be coupled to a carrier  
FT compound, with the proviso that Xaa6 and  
FT Xaa16 are not both Gly"  
FT Misc-difference 16  
FT /note= "Gly or a dextrorotatory amino acid with a  
FT side chain that can be coupled to a carrier  
FT compound, with the proviso that Xaa6 and  
FT Xaa16 are not both Gly"  
XX  
PN WO9640755-A1.  
XX  
PD 19-DEC-1996.  
XX  
PF 06-JUN-1996; 96WO-NL00223.  
XX  
PR 07-JUN-1995; 95US-0477298.  
PR 07-JUN-1995; 95US-0476013.  
XX  
PA (DLOD-) DLO INST DIERHOUDERIJ EN DIERGEZONDHEID.  
XX  
PI Meloen RH, Oonk HB;  
XX  
DR WPI; 1997-052227/05.  
XX  
PT Peptide comprising at least 2 LHRH deca-peptide sequences -  
PT contains a D-residue with side chain that can be coupled to carrier  
PT cpd., useful for porcine immuno-castration  
XX  
PS Claim 2; Page 22; 29pp; English.  
XX  
CC The sequences given in AAW21648-49 represent novel peptides which  
CC comprise at least 2 contiguous luteinising hormone releasing hormone  
CC (LHRH) decapeptide sequences, where Gly 6 of at least 1 of the  
CC decapeptides is replaced by a dextrorotatory amino acid with a side  
CC chain that can be coupled to a carrier compound. These peptides  
CC may be used in a vaccine, to inoculate an animal to effect one or more  
CC reproductive or behavioural characteristics of the animal, specifically  
CC for porcine immunocastration. Immunisation against LHRH may also be  
CC used in the treatment of prostate cancer and breast cancer and in some  
CC forms of pituitary carcinoma.  
XX  
SQ Sequence 21 AA;

Query Match 96.2%; Score 101; DB 18; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.4e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HWSYXLRPGQHWSYXLRP 18  
|||||||  
Db 2 HWSYXLRPGQHWSYXLRP 19

Search completed: June 21, 2003, 16:25:33  
Job time : 70 secs